

E. Kemmerer

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#31

OK

7/10/01

RAW SEQUENCE LISTING

DATE: 05/21/2001

PATENT APPLICATION: US/08/972,301B

TIME: 11:34:56

Input Set : A:\Seq_list.txt

Output Set: N:\CRF3\05212001\H972301B.raw

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3 <110> APPLICANT: Coleman et al.
5 <120> TITLE OF INVENTION: Endothelial Monocyte Activating Polypeptide III
7 <130> FILE REFERENCE: PF206D1
9 <140> CURRENT APPLICATION NUMBER: US 08/972,301B
10 <141> CURRENT FILING DATE: 1997-11-18
12 <150> PRIOR APPLICATION NUMBER: US 08/483,534
13 <151> PRIOR FILING DATE: 1995-06-07
15 <160> NUMBER OF SEQ ID NOS: 7
17 <170> SOFTWARE: PatentIn version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 636
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (94)..(600)
28 <400> SEQUENCE: 1
29 taccctgcc ctgaaaaaac tggccagcgc tgcctacca gatccctcaa agcagaagcc 60
31 aatggccaaa ggcctgccaa gaattcagaa cca gag gag gtc atc cca tcc cgg 114
32                                     Glu Glu Val Ile Pro Ser Arg
33                                     1               5
35 ctg gat atc cgt gtg ggg aaa atc atc act gtg gag aag cac cca gat 162
36 Leu Asp Ile Arg Val Gly Lys Ile Ile Thr Val Glu Lys His Pro Asp
37      10               15               20
39 gca gac agc ctg tat gta gag aag att gac gtg ggg gaa gct gaa cca 210
40 Ala Asp Ser Leu Tyr Val Glu Lys Ile Asp Val Gly Glu Ala Glu Pro
41      25               30               35
43 cgg act gtg gtg agc ggc ctg gta cag ttc gtg ccc aag gag gaa ctg 258
44 Arg Thr Val Val Ser Gly Leu Val Gln Phe Val Pro Lys Glu Glu Leu
45 40               45               50               55
47 cag gac agg ctg gta gtg gtg ctg tgc aac ctg aaa ccc cag aag atg 306
48 Gln Asp Arg Leu Val Val Val Leu Cys Asn Leu Lys Pro Gln Lys Met
49      60               65               70
51 aga gga gtc gag tcc caa ggc atg ctt ctg tgt gct tct ata gaa ggg 354
52 Arg Gly Val Glu Ser Gln Gly Met Leu Leu Cys Ala Ser Ile Glu Gly
53      75               80               85
55 ata aac cgc cag gtt gaa cct ctg gac cct ccg gca ggc tct gct cct 402
56 Ile Asn Arg Gln Val Glu Pro Leu Asp Pro Pro Ala Gly Ser Ala Pro
57      90               95               100
59 ggt gag cac gtg ttt gtg aag ggc tat gaa aag ggc caa cca gat gag 450
60 Gly Glu His Val Phe Val Lys Gly Tyr Glu Lys Gly Gln Pro Asp Glu
61      105               110               115
63 gag ctc aag ccc aag aag aaa gtc ttc gag aag ttg cag gct gac ttc 498
64 Glu Leu Lys Pro Lys Lys Lys Val Phe Glu Lys Leu Gln Ala Asp Phe
65 120               125               130               135
67 aaa att tct gag gag tgc atc gca cag tgg aag caa acc aac ttc atg 546
68 Lys Ile Ser Glu Glu Cys Ile Ala Gln Trp Lys Gln Thr Asn Phe Met

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69          140          145          150
71 acc aag ctg ggc tcc att tcc tgt aaa tcg ctg aaa ggg ggg aac att      594
72 Thr Lys Leu Gly Ser Ile Ser Cys Lys Ser Leu Lys Gly Gly Asn Ile
73          155          160          165
75 agc tagccagccc agcatcttcc ccccttcttc caccactga      636
76 Ser
80 <210> SEQ ID NO: 2
81 <211> LENGTH: 168
82 <212> TYPE: PRT
83 <213> ORGANISM: Homo sapiens
85 <400> SEQUENCE: 2
87 Glu Glu Val Ile Pro Ser Arg Leu Asp Ile Arg Val Gly Lys Ile Ile
88 1          5          10          15
91 Thr Val Glu Lys His Pro Asp Ala Asp Ser Leu Tyr Val Glu Lys Ile
92          20          25          30
95 Asp Val Gly Glu Ala Glu Pro Arg Thr Val Val Ser Gly Leu Val Gln
96          35          40          45
99 Phe Val Pro Lys Glu Glu Leu Gln Asp Arg Leu Val Val Val Leu Cys
100          50          55          60
103 Asn Leu Lys Pro Gln Lys Met Arg Gly Val Glu Ser Gln Gly Met Leu
104 65          70          75          80
107 Leu Cys Ala Ser Ile Glu Gly Ile Asn Arg Gln Val Glu Pro Leu Asp
108          85          90          95
111 Pro Pro Ala Gly Ser Ala Pro Gly Glu His Val Phe Val Lys Gly Tyr
112          100          105          110
115 Glu Lys Gly Gln Pro Asp Glu Glu Leu Lys Pro Lys Lys Lys Val Phe
116          115          120          125
119 Glu Lys Leu Gln Ala Asp Phe Lys Ile Ser Glu Glu Cys Ile Ala Gln
120          130          135          140
123 Trp Lys Gln Thr Asn Phe Met Thr Lys Leu Gly Ser Ile Ser Cys Lys
124 145          150          155          160
127 Ser Leu Lys Gly Gly Asn Ile Ser
128          165
131 <210> SEQ ID NO: 3
132 <211> LENGTH: 28
133 <212> TYPE: DNA
134 <213> ORGANISM: Artificial Sequence
136 <220> FEATURE:
137 <223> OTHER INFORMATION: Contains a BamHI restriction enzyme site.
139 <400> SEQUENCE: 3
140 gatcggatcc gaggaggtca tcccatcc      28
143 <210> SEQ ID NO: 4
144 <211> LENGTH: 28
145 <212> TYPE: DNA
146 <213> ORGANISM: Artificial Sequence
148 <220> FEATURE:
149 <223> OTHER INFORMATION: Contains complementary sequences to HindIII.
151 <400> SEQUENCE: 4
152 gatcaagctt ctagataatg ttccccc      28

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155 <210> SEQ ID NO: 5
156 <211> LENGTH: 28
157 <212> TYPE: DNA
158 <213> ORGANISM: Artificial Sequence
160 <220> FEATURE:
161 <223> OTHER INFORMATION: Contains a BamHI restriction enzyme site.
163 <400> SEQUENCE: 5
164 gatcggatcc gaggaggtca tcccatcc 28
167 <210> SEQ ID NO: 6
168 <211> LENGTH: 28
169 <212> TYPE: DNA
170 <213> ORGANISM: Artificial Sequence
172 <220> FEATURE:
173 <223> OTHER INFORMATION: Contains the cleavage site for the restriction endonuclease BamHI
176 <400> SEQUENCE: 6
177 gatcggatcc ctagataatg ttcccccc 28
180 <210> SEQ ID NO: 7
181 <211> LENGTH: 183
182 <212> TYPE: PRT
183 <213> ORGANISM: Homo sapiens
185 <400> SEQUENCE: 7
187 Lys Gly Glu Lys Lys Glu Lys Lys Gln Gln Ser Ile Ala Gly Ser Ala
188 1 5 10 15
190 Asp Ser Lys Pro Ile Asp Val Ser Arg Leu Asp Leu Arg Ile Gly Cys
191 20 25 30
193 Ile Ile Thr Ala Arg Lys His Pro Asp Ala Asp Ser Leu Tyr Val Glu
194 35 40 45
196 Glu Val Asp Val Gly Glu Ile Ala Pro Arg Thr Val Val Ser Gly Leu
197 50 55 60
199 Val Asn His Val Pro Leu Glu Gln Met Gln Asn Arg Met Val Ile Leu
200 65 70 75 80
202 Leu Cys Asn Leu Lys Pro Ala Lys Met Arg Gly Val Leu Ser Gln Ala
203 85 90 95
205 Met Val Met Cys Ala Ser Ser Pro Glu Lys Ile Glu Ile Leu Ala Pro
206 100 105 110
208 Pro Asn Gly Ser Val Pro Gly Asp Arg Ile Thr Phe Asp Ala Phe Pro
209 115 120 125
211 Gly Glu Pro Asp Lys Glu Leu Asn Pro Lys Lys Lys Ile Trp Glu Gln
212 130 135 140
214 Ile Gln Pro Asp Leu His Thr Asn Asp Glu Cys Val Ala Thr Tyr Lys
215 145 150 155 160
217 Gly Val Pro Phe Glu Val Lys Gly Lys Gly Val Cys Arg Ala Gln Thr
218 165 170 175
220 Met Ser Asn Ser Gly Ile Lys
221 180

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VERIFICATION SUMMARY

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